

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Burkly, Linda C  
Benjamin, Christopher D  
Hession, Catherine A  
Whitty, Adrian
- (ii) TITLE OF INVENTION: COMMON GAMMA CHAIN BLOCKING AGENTS
- (iii) NUMBER OF SEQUENCES: 17
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Biogen, Inc.
  - (B) STREET: 14 Cambridge Center
  - (C) CITY: Cambridge
  - (D) STATE: Massachusetts
  - (E) COUNTRY: USA
  - (F) ZIP: 02142
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER: A006 PCT CIP
  - (B) FILING DATE: 09-MAY-1997
  - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 60/017,466
  - (B) FILING DATE: 10-MAY-1996
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: Kaplan, Warren A.
  - (B) REGISTRATION NUMBER: 34,199
  - (C) REFERENCE/DOCKET NUMBER: A006 PCT CIP
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: 617 679-2000
  - (B) TELEFAX: 617 679-2838

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1446 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO
- (vii) IMMEDIATE SOURCE:
  - (B) CLONE: pLB001

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGGTGAAGC CATCATTACC ATTACATCC CTCTTATTCC TGCAGCTGCC CCTGCTGGGA	60
GTGGGGCTGA ACACGACAAT TCTGACGCCC AATGGGAATG AAGACACCAC AGCTGATTTTC	120
TTCTTGACCA CTATGCCCAC TGA CTCCCTC AGTGTTTCCA CTCTGCCCCCT CCCAGAGGTT	180
CAGTGTTTTG TGTTCAATGT CGAGTACATG AATTGCACTT GGAACAGCAG CTCTGAGCCC	240
CAGCCTACCA ACCTCACTCT GCATTATTGG TACAAGAACT CGGATAATGA TAAAGTCCAG	300
AAGTGCAGCC ACTATCTATT CTCTGAAGAA ATCACTTCTG GCTGTCA GTT GCAAAAAAAG	360
GAGATCCACC TCTACCAAAC ATTTGTTGTT CAGCTCCAGG ACCCACGGGA ACCCAGGAGA	420
CAGGCCACAC AGATGCTAAA ACTGCAGAAT CTGGTGATCC CCTGGGCTCC AGAGAACCTA	480
ACACTTCACA AACTGAGTGA ATCCCAGCTA GAACTGAACT GGAACAACAG ATTCTTGAAC	540
CACTGTTTGG AGCACTTGGT GCAGTACCGG ACTGACTGGG ACCACAGCTG GACTGAACAA	600
TCAGTGGAAT ATAGACATAA GTTCTCCTTG CCTAGTGTGG ATGGGCAGAA ACGCTACATG	660
TTTCGTGTTT GGAGCCGCTT TAACCCACTC TGTGGAAGTG CTCAGCATTG GAGTGAATGG	720
AGCCACCCAA TCCACTGGGG GAGCAATACT TCAAAAGAGA ATGTCGACAA AACTCACACA	780
TGCCCACCGT GCCCAGCACC TGAACCTCTG GGGGGACCGT CAGTCTTCCT CTTCCCCCCA	840
AAACCCAAGG ACACCCTCAT GATCTCCCGG ACCCCTGAGG TCACATGCGT GGTGGTGGAC	900
GTGAGCCACG AAGACCCTGA GGTCAAGTTC AACTGGTACG TGGACGGCGT GGAGGTGCAT	960
AATGCCAAGA CAAAGCCGCG GGAGGAGCAG TACAACAGCA CGTACCGTGT GGTGAGCGTC	1020
CTCACCCTCC TGCACCAGGA CTGGCTGAAT GGCAAGGAGT ACAAGTGCAA GGTCTCCAAC	1080
AAAGCCCTCC CAGCCCCCAT CGAGAAAACC ATCTCCAAAG CCAAAGGGCA GCCCCGAGAA	1140
CCACAGGTGT ACACCCTGCC CCCATCCCGG GATGAGCTGA CCAAGAACCA GGTGAGCCTG	1200
ACCTGCCTGG TCAAAGGCTT CTATCCCAGC GACATCGCCG TGGAGTGGGA GAGCAATGGG	1260
CAGCCGGAGA ACAACTACAA GACCACGCCT CCCGTGTTGG ACTCCGACGG CTCCTTCTTC	1320
CTCTACAGCA AGCTCACCCT GGACAAGAGC AGGTGGCAGC AGGGGAACGT CTTCTCATGC	1380
TCCGTGATGC ATGAGGCTCT GCACAACCAC TACACGAGA AGAGCCTCTC CCTGTCTCCG	1440
GGTAAA	1446

## (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 482 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Val	Lys	Pro	Ser	Leu	Pro	Phe	Thr	Ser	Leu	Leu	Phe	Leu	Gln	Leu
1				5					10					15	
Pro	Leu	Leu	Gly	Val	Gly	Leu	Asn	Thr	Thr	Ile	Leu	Thr	Pro	Asn	Gly
			20					25					30		
Asn	Glu	Asp	Thr	Thr	Ala	Asp	Phe	Phe	Leu	Thr	Thr	Met	Pro	Thr	Asp
		35					40					45			
Ser	Leu	Ser	Val	Ser	Thr	Leu	Pro	Leu	Pro	Glu	Val	Gln	Cys	Phe	Val
	50					55					60				
Phe	Asn	Val	Glu	Tyr	Met	Asn	Cys	Thr	Trp	Asn	Ser	Ser	Ser	Glu	Pro
65					70					75					80
Gln	Pro	Thr	Asn	Leu	Thr	Leu	His	Tyr	Trp	Tyr	Lys	Asn	Ser	Asp	Asn
				85					90					95	
Asp	Lys	Val	Gln	Lys	Cys	Ser	His	Tyr	Leu	Phe	Ser	Glu	Glu	Ile	Thr
			100					105					110		
Ser	Gly	Cys	Gln	Leu	Gln	Lys	Lys	Glu	Ile	His	Leu	Tyr	Gln	Thr	Phe
		115					120					125			
Val	Val	Gln	Leu	Gln	Asp	Pro	Arg	Glu	Pro	Arg	Arg	Gln	Ala	Thr	Gln
	130					135					140				
Met	Leu	Lys	Leu	Gln	Asn	Leu	Val	Ile	Pro	Trp	Ala	Pro	Glu	Asn	Leu
145					150					155					160
Thr	Leu	His	Lys	Leu	Ser	Glu	Ser	Gln	Leu	Glu	Leu	Asn	Trp	Asn	Asn
				165					170					175	
Arg	Phe	Leu	Asn	His	Cys	Leu	Glu	His	Leu	Val	Gln	Tyr	Arg	Thr	Asp
			180					185					190		
Trp	Asp	His	Ser	Trp	Thr	Glu	Gln	Ser	Val	Asp	Tyr	Arg	His	Lys	Phe
		195					200					205			
Ser	Leu	Pro	Ser	Val	Asp	Gly	Gln	Lys	Arg	Tyr	Met	Phe	Arg	Val	Arg
	210					215					220				
Ser	Arg	Phe	Asn	Pro	Leu	Cys	Gly	Ser	Ala	Gln	His	Trp	Ser	Glu	Trp
225					230					235					240
Ser	His	Pro	Ile	His	Trp	Gly	Ser	Asn	Thr	Ser	Lys	Glu	Asn	Val	Asp
				245					250					255	
Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly
			260					265					270		
Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	Met	Ile
		275					280					285			
Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	His	Glu
	290					295					300				
Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	Val	His
305					310					315					320

[illegible]

(2) INFORMATION FOR SEQ ID NO:3:

**(i) SEQUENCE CHARACTERISTICS:**

- (A) LENGTH: 112 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Leu 1	Gln	Glu	Ser	Gly 5	Pro	Gly	Leu	Val	Ala 10	Pro	Ser	Gln	Ser	Leu 15	Ser
Ile	Thr	Cys	Thr 20	Val	Ser	Gly	Phe	Ser 25	Leu	Thr	Ser	Tyr	Gly 30	Val	His
Trp	Val	Arg 35	Gln	Pro	Pro	Gly	Lys 40	Gly	Leu	Glu	Trp	Leu 45	Gly	Val	Ile
Trp	Ala 50	Gly	Gly	Ser	Thr	Asn 55	Tyr	Asn	Ser	Ala	Leu 60	Met	Ser	Arg	Leu
Asn 65	Ile	Asn	Arg	Asp 70	Asn	Ser	Lys	Ser	Gln	Ile 75	Phe	Leu	Lys	Met	Asn 80

Ser Leu Gln Thr Asp Asp Thr Ala Ile Tyr Tyr Cys Ala Arg Glu Gly  
                                     85                                    90                                    95  
 Ser Thr Val Asp Ser Met Asp Tyr Trp Gly Gln Gly Thr Thr Val Thr  
                                     100                                    105                                    110

## (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 106 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Asp Ile Val Met Thr Gln Ser His Lys Phe Met Ser Thr Ser Val Gly  
 1                                    5                                    10                                    15  
 Asp Ser Ile Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Thr Thr Ala  
                                     20                                    25                                    30  
 Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile  
                                     35                                    40                                    45  
 Tyr Trp Ala Ser Thr Arg His Thr Gly Val Pro Asp Arg Phe Thr Gly  
                                     50                                    55                                    60  
 Ser Gly Ser Gly Thr Asp Tyr Thr Leu Thr Ile Ser Ser Val Gln Ala  
                                     65                                    70                                    75                                    80  
 Glu Asp Leu Ala Leu Tyr Tyr Cys Gln Gln His Tyr Ile Thr Pro Trp  
                                     85                                    90                                    95  
 Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile  
                                     100                                    105

## (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 319 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GATATCGTAA TGACCCAGTC TCACAAATTC ATGTCCACAT CAGTAGGAGA CAGTATCACC	60
ATCACCTGCA AGGCCAGTCA GGATGTGACT ACTGCTGTAG CCTGGTATCA ACAAAAACCA	120
GGGCAATCTC CTAAACTTCT GATTTACTGG GCATCCAGCC GGCACACTGG AGTCCCTGAT	180

CGCTTCACAG GCAGTGGATC TGGGACAGAT TATACTCTCA CCATCAGCAG TGTGCAGGCT 240  
 GAAGACCTGG CACTTTATTA CTGTCAGCAA CATTATATCA CTCCGTGGAC GTTCGGTGGA 300  
 GGGACCAAGC TGGAGATCT 319

## (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 336 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CTGCAGGAGT CAGGACCTGG CCTGGTGGCG CCCTCACAGA GCCTGTCCAT CACTTGCACT 60  
 GTCTCTGGGT TTTCATTAAC CAGCTATGGT GTACACTGGG TTCGCCAGCC TCCAGGAAAG 120  
 GGTCTGGAGT GGCTGGGAGT CATTTGGGCT GGTGGAAGCA CAAATTATAA TTCGGCTCTC 180  
 ATGTCCAGAC TGAACATCAA CAGAGACAAT TCCAAGAGCC AAATTTTCTT AAAAATGAAC 240  
 AGTCTGCAAA CTGATGACAC AGCCATCTAC TACTGTGCCA GAGAGGGTTC TACGGTAGAT 300  
 TCTATGGACT ACTGGGGCCA AGGGACCACG GTCACC 336

## (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 36 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AACTGCAGCG GCCGCGATGG TGAAGCCATC ATTACC 36

## (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 32 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GACTTTGTCTG ACATTCTCTT TTGAAGTATT GC 32

## (2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CTGGATATCG TAATGACCCA GTCTCCA

27

## (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTTAGATCTC CAGCTTGGTC CC

22

## (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Ala	Gly	Gly	Thr	Ser	Met	Ala	Arg	Cys	Thr	Gly	Cys	Ala	Gly	Ser	Ala
1					5				10					15	

Gly	Thr	Cys	Trp	Gly	Gly
				20	

## (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 32 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TGAGGAGACG GTGACCGTGG TCCCTTGGCC CC

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 5 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Phe Asn Val Glu Tyr  
1 5

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Lys Glu Ile His Leu Tyr Gln  
1 5

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 7 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: not relevant
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Leu Gln Asn Leu Val Ile Pro  
1 5



(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 5 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: not relevant  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

His Cys Leu Glu His  
1 5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

Phe Asn Pro  
1

[illegible]